

RAW SEQUENCE LISTING

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Application Serial Number: 10/774,018

Source: IFW0

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/774,018

DATE: 10/20/2004
TIME: 16:28:37

Input Set : A:\HENK0060.ST25.txt
Output Set: N:\CRF4\10202004\J774018.raw

3 <110> APPLICANT: Kottwitz, Beatrix
 4 Breves, Roland
 5 Maurer, Karl-Heinz
 7 <120> TITLE OF INVENTION: DETERGENT AND CLEANING AGENT WITH HYBRID ALPHA-AMYLASES
 9 <130> FILE REFERENCE: HENK-0060 / H4714
 11 <140> CURRENT APPLICATION NUMBER: US 10/774,018
 12 <141> CURRENT FILING DATE: 2004-02-06
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP02/08391
 15 <151> PRIOR FILING DATE: 2002-07-27
 17 <150> PRIOR APPLICATION NUMBER: EP 101 38 753.9
 18 <151> PRIOR FILING DATE: 2001-08-07
 20 <160> NUMBER OF SEQ ID NOS: 20
 22 <170> SOFTWARE: PatentIn version 3.3
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1452
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Bacillus licheniformis
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(1449)
 34 <400> SEQUENCE: 1
 35 gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc 48
 36 Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 37 1 5 10 15
 39 aat gac ggc caa cat tgg aag cgc ttg caa aac gac tcg gca tat ttg 96
 40 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu
 41 20 25 30
 43 gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga 144
 44 Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 45 35 40 45
 47 acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta 192
 48 Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 49 50 55 60
 51 ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa 240
 52 Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 53 65 70 75 80
 55 gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac 288
 56 Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
 57 85 90 95
 59 gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat ggc acc 336
 60 Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
 61 100 105 110
 63 gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta 384

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64	Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val			
65	115	120	125	
67	att tca gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg	432		
68	Ile Ser Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro			
69	130	135	140	
71	ggg cgc ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt	480		
72	Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe			
73	145	150	155	160
75	gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag	528		
76	Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys			
77	165	170	175	
79	ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac	576		
80	Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn			
81	180	185	190	
83	tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc	624		
84	Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val			
85	195	200	205	
87	gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa	672		
88	Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln			
89	210	215	220	
91	ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt	720		
92	Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe			
93	225	230	235	240
95	ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg	768		
96	Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met			
97	245	250	255	
99	ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac	816		
100	Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn			
101	260	265	270	
103	tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt	864		
104	Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu			
105	275	280	285	
107	cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg	912		
108	His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Tyr Asp Met			
109	290	295	300	
111	agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg	960		
112	Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala			
113	305	310	315	320
115	gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag	1008		
116	Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu			
117	325	330	335	
119	tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct gct ttt att ctc	1056		
120	Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu			
121	340	345	350	
123	aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg	1104		
124	Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly			
125	355	360	365	
127	acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att	1152		
128	Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu His Lys Ile			

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129	370	375	380	
131	gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat			1200
132	Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His			
133	385	390	395	400
135	gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac			1248
136	Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp			
137	405	410	415	
139	agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc			1296
140	Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro			
141	420	425	430	
143	ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca			1344
144	Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr			
145	435	440	445	
147	tgg cat gac att acc gga aac cgt tcg gag cgc gtt gtc atc aat tcg			1392
148	Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser			
149	450	455	460	
151	gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat			1440
152	Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr			
153	465	470	475	480
155	gtt caa aga tag			1452
156	Val Gln Arg			
160	<210> SEQ ID NO: 2			
161	<211> LENGTH: 483			
162	<212> TYPE: PRT			
163	<213> ORGANISM: Bacillus licheniformis			
165	<400> SEQUENCE: 2			
167	Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro			
168	1	5	10	15
171	Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu			
172	20	25	30	
175	Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly			
176	35	40	45	
179	Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu			
180	50	55	60	
183	Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys			
184	65	70	75	80
187	Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn			
188	85	90	95	
191	Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Ala Asp Ala Thr			
192	100	105	110	
195	Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val			
196	115	120	125	
199	Ile Ser Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro			
200	130	135	140	
203	Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe			
204	145	150	155	160
207	Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys			
208	165	170	175	
211	Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn			

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212	180	185	190	
215	Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val			
216	195	200	205	
219	Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln			
220	210	215	220	
223	Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe			
224	225	230	235	240
227	Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met			
228	245	250	255	
231	Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn			
232	260	265	270	
235	Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu			
236	275	280	285	
239	His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Tyr Asp Met			
240	290	295	300	
243	Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala			
244	305	310	315	320
247	Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu			
248	325	330	335	
251	Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu			
252	340	345	350	
255	Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly			
256	355	360	365	
259	Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile			
260	370	375	380	
263	Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His			
264	385	390	395	400
267	Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp			
268	405	410	415	
271	Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro			
272	420	425	430	
275	Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr			
276	435	440	445	
279	Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser			
280	450	455	460	
283	Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr			
284	465	470	475	480
287	Val Gln Arg			
291	<210> SEQ ID NO: 3			
292	<211> LENGTH: 1452			
293	<212> TYPE: DNA			
294	<213> ORGANISM: Bacillus amyloliquefaciens			
297	<220> FEATURE:			
298	<221> NAME/KEY: CDS			
299	<222> LOCATION: (1)..(1449)			
301	<400> SEQUENCE: 3			
302	gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac		48	
303	Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp			
304	1	5	10	15

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306	ggc	cag	cat	tgg	aaa	cga	ttg	cag	aat	gat	gcg	gaa	cat	tta	tcg	gat	96
307	Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp	
308				20				25						30			
310	atc	gga	atc	act	gcc	gtc	tgg	att	cct	ccc	gca	tac	aaa	gga	ttg	agc	144
311	Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Leu	Ser	
312					35				40			45					
314	caa	tcc	gat	aac	gga	tac	gga	cct	tat	gat	ttg	tat	gat	tta	gga	gaa	192
315	Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	Glu
316					50				55			60					
318	ttc	cag	caa	aaa	ggg	acg	gtc	aga	acg	aaa	tac	ggc	aca	aaa	tca	gag	240
319	Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Ser	Glu	
320	65				70				75			80					
322	ctt	caa	gat	gcf	atc	ggc	tca	ctg	cat	tcc	cg	aac	gtc	caa	gta	tac	288
323	Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	Val	Tyr	
324					85				90			95					
326	gga	gat	gtg	gtt	ttg	aat	cat	aag	gct	ggt	gct	gat	gca	aca	gaa	gat	336
327	Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp	
328					100				105			110					
330	gta	act	gcc	gtc	gaa	gtc	aat	ccg	gcc	aat	aga	aat	cag	gaa	act	tcc	384
331	Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu	Thr	Ser	
332					115				120			125					
334	gag	gaa	tat	caa	atc	aaa	gcg	tgg	acg	gat	ttt	cgt	ttt	ccg	ggc	cgt	432
335	Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	Gly	Arg	
336					130				135			140					
338	gga	aac	acg	tac	agt	gat	ttt	aaa	tgg	cat	tgg	tat	cat	ttc	gac	gga	480
339	Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	
340	145				150				155			160					
342	gcg	gac	tgg	gat	gaa	tcc	cg	aag	atc	acg	cgc	atc	ttt	aag	ttt	cgt	528
343	Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	Phe	Arg	
344					165				170			175					
346	ggg	gaa	gga	aaa	gcg	tgg	gat	tgg	gaa	gta	tca	agt	gaa	aac	ggc	aac	576
347	Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	Gly	Asn	
348					180				185			190					
350	tat	gac	tat	tta	atg	tat	gct	gat	ttt	gac	tac	gac	cac	cct	gat	gtc	624
351	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	Asp	Val	
352					195				200			205					
354	gtg	gca	gag	aca	aaa	aaa	tgg	ggt	atc	tgg	tat	gcg	aat	gaa	ctg	tca	672
355	Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser	
356					210				215			220					
358	tta	gac	ggc	tcc	cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	tca	ttt	720
359	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe	
360	225				230				235			240					
362	ctg	cgt	gat	tgg	gtt	cag	gcf	gtc	aga	cag	gcf	acg	gga	aaa	gaa	atg	768
363	Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met	
364					245				250			255					
366	ttt	acg	gtt	gcf	gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	gaa	aac	816
367	Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn	
368					260				265			270					
370	tac	ttg	aat	aaa	aca	acg	ttt	aat	caa	tcc	gtg	ttt	gat	gtt	ccg	ttt	864

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valid <213> Response:

use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823 (b) of New Sequence Rules. Valid response is Artificial Sequence.

Q#:5,6,7,8,9,10,11,12,13,14,15,16,17,18

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